```
         10                  30
atgacgactgaaccgttatttttcaagcctgttttcaaagaaagaatt
M  T  T  E  P  L  F  F  K  P  V  F  K  E  R  I

50                  70                  90
tggggcgggaccgctttagctgattttggctataccattccgtcacaa
W  G  G  T  A  L  A  D  F  G  Y  T  I  P  S  Q

           110                 130
cgaacaggggagtgctgggcttttgccgcgcatcaaaatggtcaaagc
R  T  G  E  C  W  A  F  A  A  H  Q  N  G  Q  S

   150                 170                 190
gttgttcaaaacggaatgtataaggggttcacgctcagcgaattatgg
V  V  Q  N  G  M  Y  K  G  F  T  L  S  E  L  W

                210                 230
gaacatcacagacatttattcggacagcttgaaggggaccgtttccct
E  H  H  R  H  L  F  G  Q  L  E  G  D  R  F  P

         250                 270                 2
ctgcttacaaaaatattagatgctgaccaggacttatctgttcaggtg
L  L  T  K  I  L  D  A  D  Q  D  L  S  V  Q  V

90                  310                 330
catccgaatgatgaatatgccaacatacatgaaaacggtgagcttgga
H  P  N  D  E  Y  A  N  I  H  E  N  G  E  L  G

           350                 370
aaaacagaatgctggtacattattgattgccaaaaagatgccgagatt
K  T  E  C  W  Y  I  I  D  C  Q  K  D  A  E  I

   390                 410                 430
atttatggccacaatgcaacaacaaaggaagaactaactaccatgata
I  Y  G  H  N  A  T  T  K  E  E  L  T  T  M  I

                450                 470
gagcgtggagaatgggatgagctcttgcgccgtgtaaaggtaaagccg
E  R  G  E  W  D  E  L  L  R  R  V  K  V  K  P

         490                 510                 5
ggggatttttctatgtgccaagcggtactgttcatgcgattggaaaa
G  D  F  F  Y  V  P  S  G  T  V  H  A  I  G  K

30                  550                 570
ggaattcttgctttggagacgcagcagaactcagacacaacctacaga
G  I  L  A  L  E  T  Q  Q  N  S  D  T  T  Y  R
```

FIG._1A

```
          590                       610
ttatatgattatgaccgaaaagatgcagaaggcaagctgcgcgagctt
L  Y  D  Y  D  R  K  D  A  E  G  K  L  R  E  L

   630                    650                    670
catctgaaaaagagcattgaagtgatagaggtcccgtctattccagaa
H  L  K  K  S  I  E  V  I  E  V  P  S  I  P  E

                690                    710
cggcatacagttcaccatgaacaaattgaggatttgcttacaacgaca
R  H  T  V  H  H  E  Q  I  E  D  L  L  T  T  T

       730                    750                   7
ttgattgaatgcgcttacttttcggtggggaaatggaacttatcagga
L  I  E  C  A  Y  F  S  V  G  K  W  N  L  S  G

70                    790                    810
tcagcaagcttaaagcagcaaaaaccattccttcttatcagtgtgatt
S  A  S  L  K  Q  Q  K  P  F  L  L  I  S  V  I

          830                    850
gaaggggagggccgtatgatctctggtgagtatgtctatcctttcaaa
E  G  E  G  R  M  I  S  G  E  Y  V  Y  P  F  K

   870                    890                    910
aaaggagatcatatgttgctgccttacggtcttggagaatttaaactc
K  G  D  H  M  L  L  P  Y  G  L  G  E  F  K  L

                930
gaaggatatgcagaatgtatcgtctcccatctg
E  G  Y  A  E  C  I  V  S  H  L
```

FIG._1B

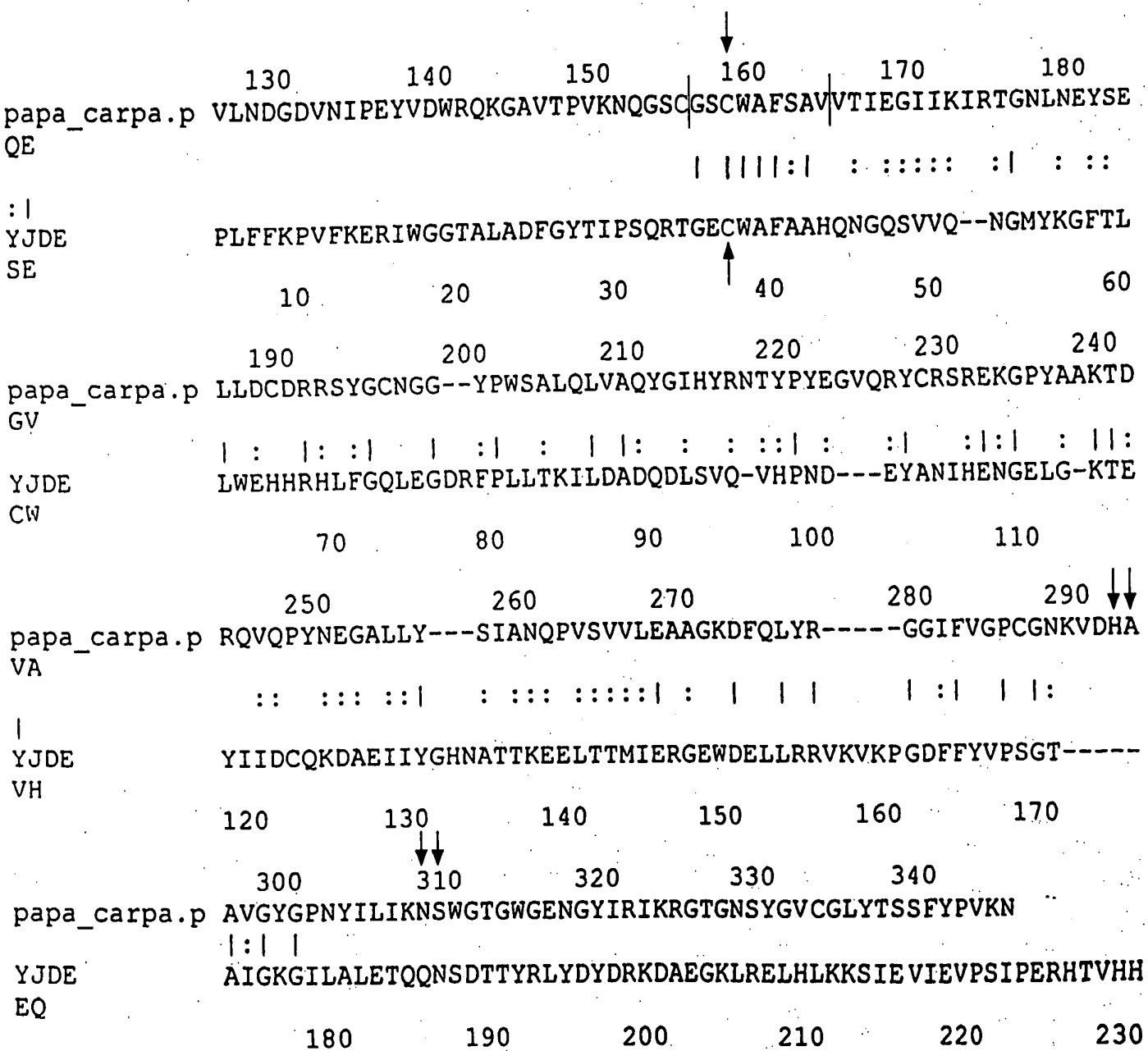

FIG._2

Proteases from Gram-Positive Organisms
David A. Estell
SN# Unassigned
Docket No. GC381-US-D1
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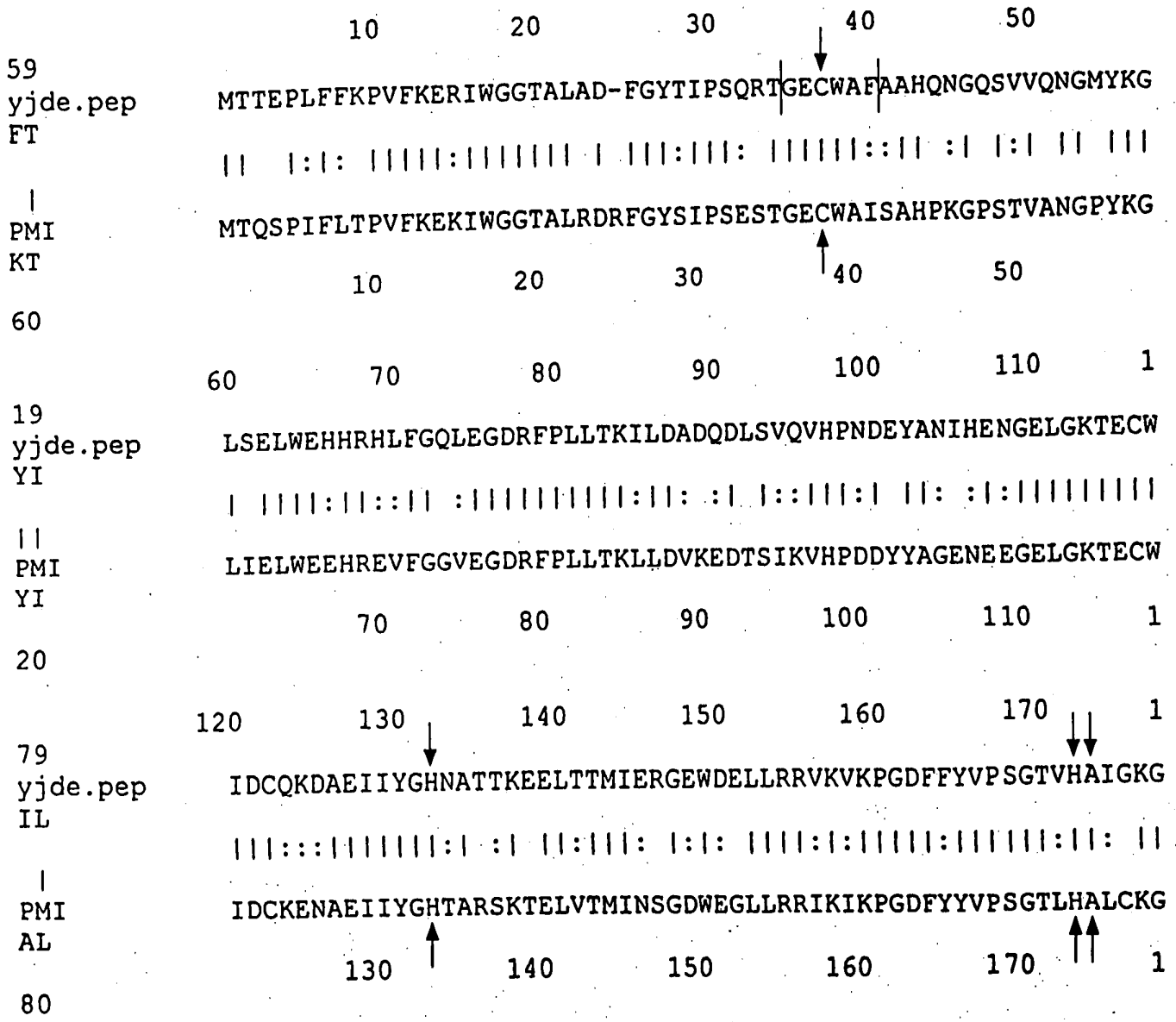
10 20 30 40 50
59
yjde.pep MTTEPLFFKPVFKERIWGGTALAD-FGYTIPSQRTGECWAFAAHQNGQSVVQNGMYKG
FT
PMI MTQSPIFLTPVFKEKIWGGTALRDRFGYSIPSESTGECWAISAHPKGPSTVANGPYKG
KT
10 20 30 40 50
60
60 70 80 90 100 110 1
19
yjde.pep LSELWEHHRHLFGQLEGDRFPLLTKILDADQDLSVQVHPNDEYANIHENGELGKTECW
YI
PMI LIELWEEHREVFGGVEGDRFPLLTKLLDVKEDTSIKVHPDDYYAGENEEGELGKTECW
YI
70 80 90 100 110 1
20
120 130 140 150 160 170 1
79
yjde.pep IDCQKDAEIIYGHNATTKEELTTMIERGEWDELLRRVKVKPGDFFYVPSGTVHAIGKG
IL
PMI IDCKENAEIIYGHTARSKTELVTMINSGDWEGLLRRIKIKPGDFYYVPSGTLHALCKG
AL
130 140 150 160 170 1
80

FIG._3A

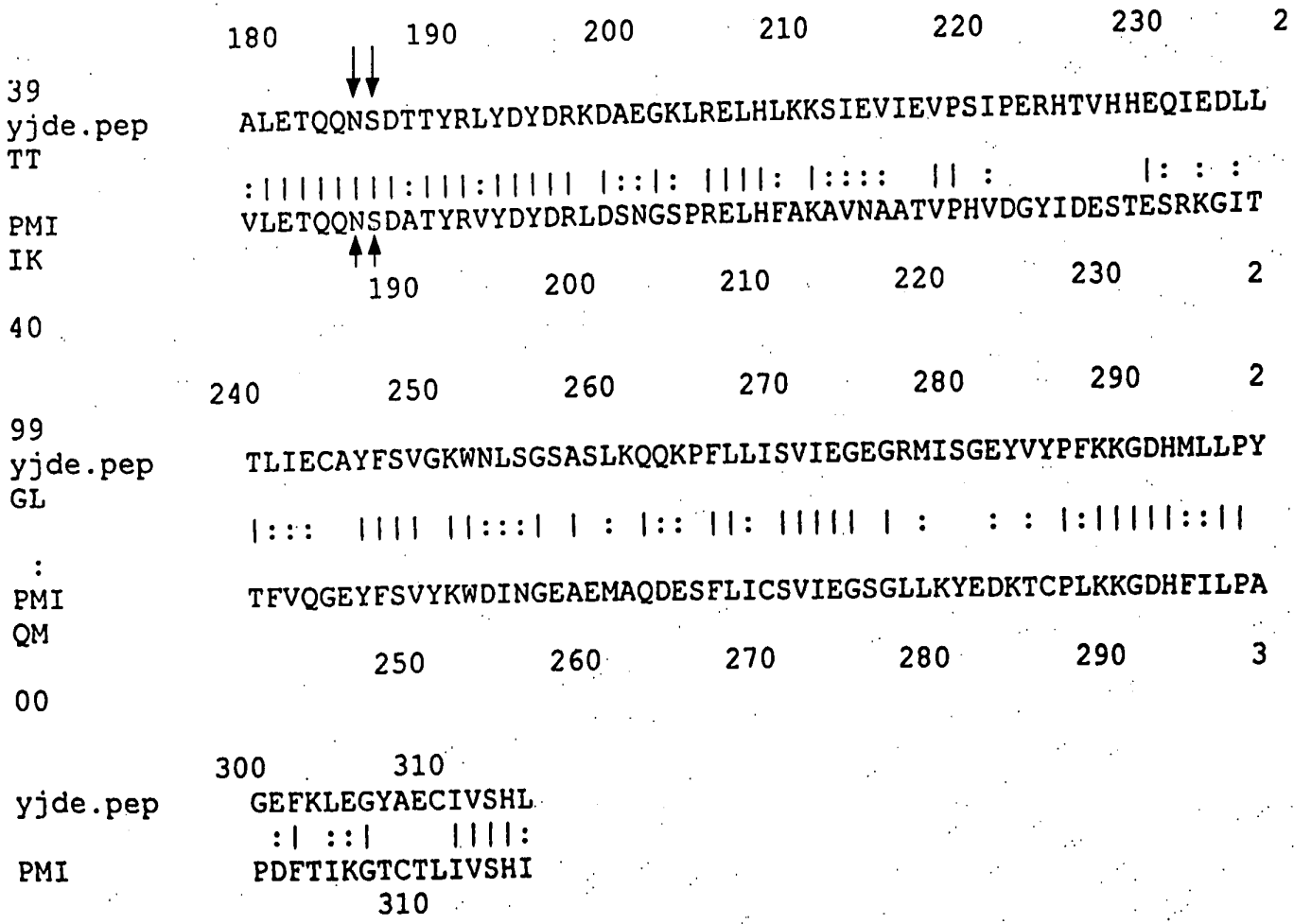
180 190 200 210 220 230 2
39
yjde.pep ALETQQNSDTTYRLYDYDRKDAEGKLRELHLKKSIEVIEVPSIPERHTVHHEQIEDLL
TT
PMI VLETQQNSDATYRVYDYDRLDSNGSPRELHFAKAVNAATVPHVDGYIDESTESRKGIT
IK
190 200 210 220 230 2
40
240 250 260 270 280 290 2
99
yjde.pep TLIECAYFSVGKWNLSGSASLKQQKPFLLISVIEGEGRMISGEYVYPFKKGDHMLLPY
GL
PMI TFVQGEYFSVYKWDINGEAEMAQDESFLICSVIEGSGLLKYEDKTCPLKKGDHFILPA
QM
250 260 270 280 290 3
00
300 310
yjde.pep GEFKLEGYAECIVSHL
PMI PDFTIKGTCTLIVSHI
310

FIG._3B

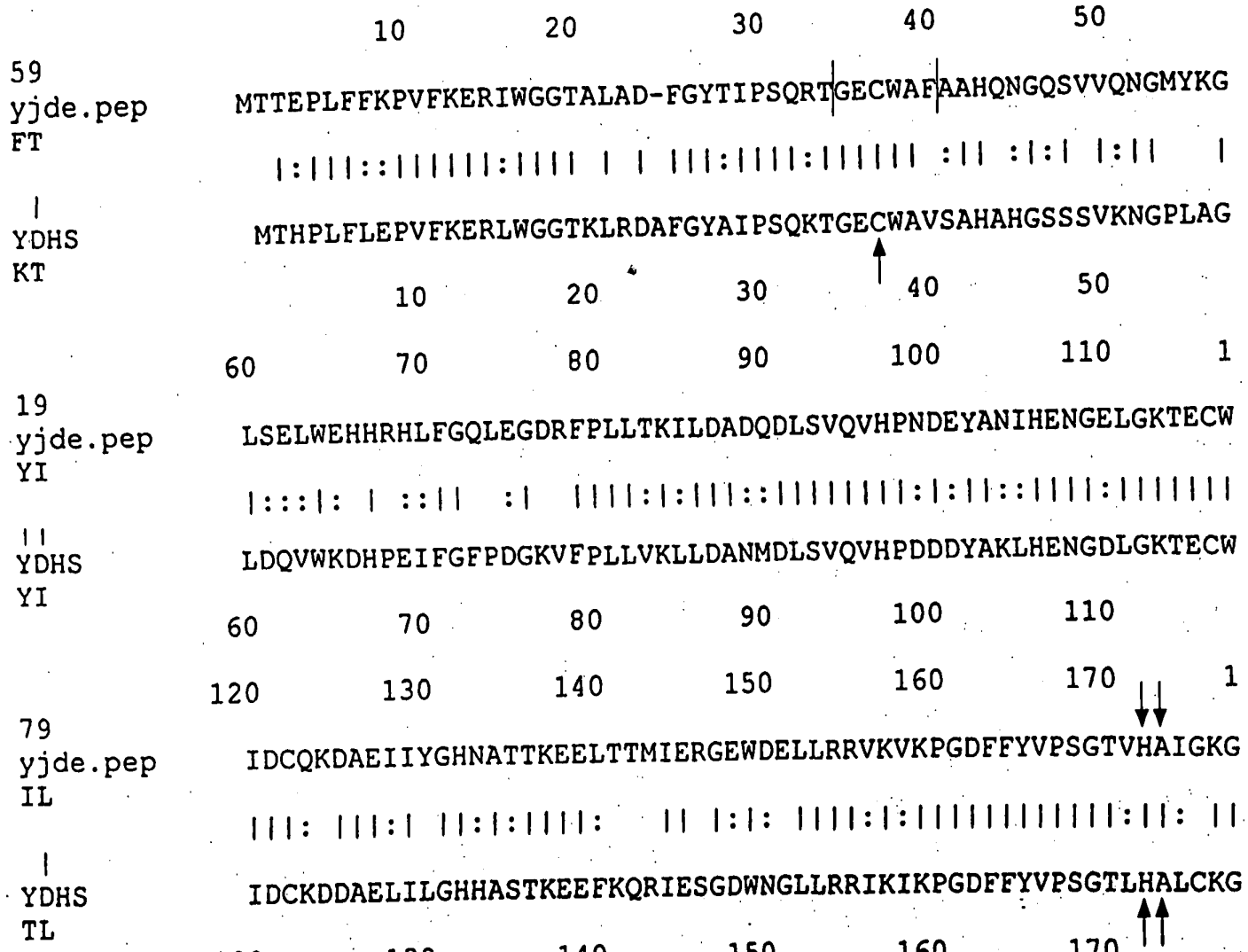
10 20 30 40 50
59
yjde.pep MTTEPLFFKPVFKERIWGGTALAD-FGYTIPSQRTGECWAFAAHQNGQSVVQNGMYKG
FT
YDHS MTHPLFLEPVFKERLWGGTKLRDAFGYAIPSQKTGECWAVSAHAHGSSSVKNGPLAG
KT
10 20 30 40 50
60 70 80 90 100 110 1
19
yjde.pep LSELWEHHRHLFGQLEGDRFPLLTKILDADQDLSVQVHPNDEYANIHENGELGKTECW
YI
YDHS LDQVWKDHPEIFGFPDGKVFPLLVKLLDANMDLSVQVHPDDDYAKLHENGDLGKTECW
YI
60 70 80 90 100 110
120 130 140 150 160 170 1
79
yjde.pep IDCQKDAEIIYGHNATTKEELTTMIERGEWDELLRRVKVKPGDFFYVPSGTVHAIGKG
IL
YDHS IDCKDDAELILGHHASTKEEFKQRIESGDWNGLLRRIKIKPGDFFYVPSGTLHALCKG
TL
120 130 140 150 160 170

FIG._4A

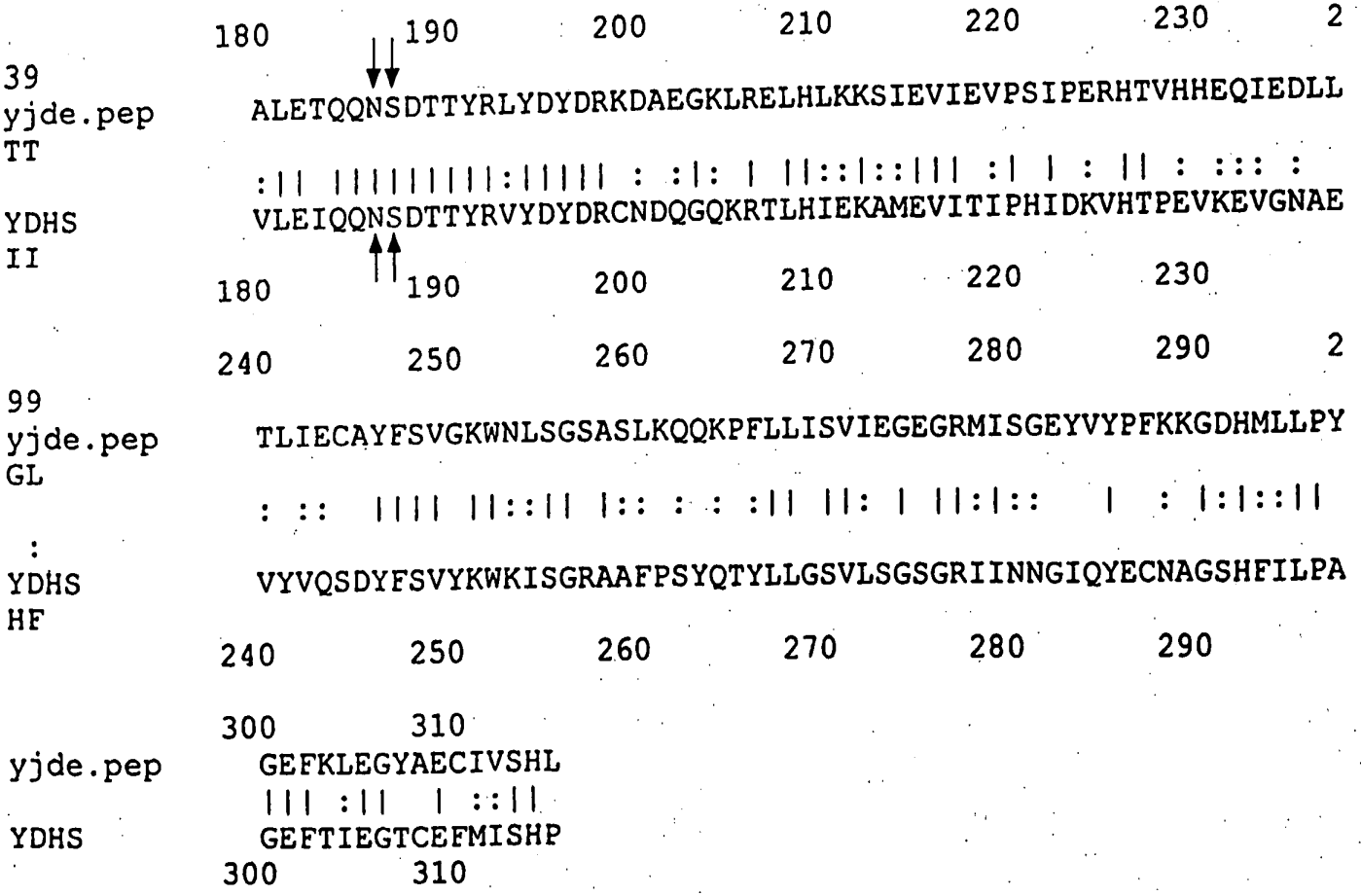
180 190 200 210 220 230 2
39
yjde.pep ALETQQNSDTTYRLYDYDRKDAEGKLRELHLKKSIEVIEVPSIPERHTVHHEQIEDLL
TT
YDHS VLEIQQNSDTTYRVYDYDRCNDQGQKRTLHIEKAMEVITIPHIDKVHTPEVKEVGNAE
II
180 190 200 210 220 230
240 250 260 270 280 290 2
99
yjde.pep TLIECAYFSVGKWNLSGSASLKQQKPFLLISVIEGEGRMISGEYVYPFKKGDHMLLPY
GL
YDHS VYVQSDYFSVYKWKISGRAAFPSYQTYLLGSVLSGSGRIINNGIQYECNAGSHFILPA
HF
240 250 260 270 280 290
300 310
yjde.pep GEFKLEGYAECIVSHL
YDHS GEFTIEGTCEFMISHP
300 310

FIG._4B

```
        10                  30
atgacgcatccattattttagagcctgtctttaaagaaagactatgg
M  T  H  P  L  F  L  E  P  V  F  K  E  R  L  W

50                  70                  90
ggagggacgaagcttcgtgacgcttttggctacgcaataccctcacaa
G  G  T  K  L  R  D  A  F  G  Y  A  I  P  S  Q

          110                 130
aaaacaggtgagtgctgggccgtttctgcacatgcccatggctcgtcg
K  T  G  E  C  W  A  V  S  A  H  A  H  G  S  S

   150                 170                 190
tctgtaaaaaatggcccgctggcaggaaagacacttgatcaagtatgg
S  V  K  N  G  P  L  A  G  K  T  L  D  Q  V  W

                210                 230
aaagatcatccagagatattcgggtttccggatggtaaggtgtttccg
K  D  H  P  E  I  F  G  F  P  D  G  K  V  F  P

       250                 270                  2
ctgctggtaaagctgctggacgccaatatggatctctccgtgcaagtc
L  L  V  K  L  L  D  A  N  M  D  L  S  V  Q  V

90                  310                 330
catcctgatgatgattatgcaaaactgcacgaaaatggcgaccttggt
H  P  D  D  D  Y  A  K  L  H  E  N  G  D  L  G

          350                 370
aaaacggagtgctggtatatcattgattgcaaagatgacgccgaacta
K  T  E  C  W  Y  I  I  D  C  K  D  D  A  E  L

   390                 410                 430
attttgggacatcatgcaagcacaaaggaagagttcaaacaacgaata
I  L  G  H  H  A  S  T  K  E  E  F  K  Q  R  I

                450                 470
gaaagcggtgattggaacgggctgctgaggcgaatcaaaatcaagcca
E  S  G  D  W  N  G  L  L  R  R  I  K  I  K  P

       490                 510                  5
ggagatttcttttatgtgccaagcggtacactccatgctttatgtaag
G  D  F  F  Y  V  P  S  G  T  L  H  A  L  C  K

30                  550                 570
ggaacccttgtccttgaaatccagcaaaactctgatacaacatatcgc
G  T  L  V  L  E  I  Q  Q  N  S  D  T  T  Y  R
```

FIG._5A

```
                590                                610
gtatacgattatgaccgctgtaatgaccagggccaaaaaagaactctt
V  Y  D  Y  D  R  C  N  D  Q  G  Q  K  R  T  L

   630                  650                  670
catatagaaaaagccatggaagtcataacgataccgcatatcgataaa
H  I  E  K  A  M  E  V  I  T  I  P  H  I  D  K

                690                  710
gtgcatacaccggaagtaaaagaagttggtaacgctgagatcattgtt
V  H  T  P  E  V  K  E  V  G  N  A  E  I  I  V

       730                  750                  7
tatgtgcaatcagattatttctcagtgtacaaatggaagattagcggc
Y  V  Q  S  D  Y  F  S  V  Y  K  W  K  I  S  G

70                  790                  810
cgagctgcttttccttcatatcaaacctatttgctggggagtgttctg
R  A  A  F  P  S  Y  Q  T  Y  L  L  G  S  V  L

            830                  850
agcggatcaggacgaatcataaataatggtattcagtatgaatgcaat
S  G  S  G  R  I  I  N  N  G  I  Q  Y  E  C  N

   870                  890                  910
gcaggctcacactttattctgcctgcgcattttggagaatttacaata
A  G  S  H  F  I  L  P  A  H  F  G  E  F  T  I

                930
gaaggaacatgtgaattcatgatatctcatcct
E  G  T  C  E  F  M  I  S  H  P
```

FIG._5B

```
          10                                  30
atgacgcaatcaccgatttttctaacgcctgtgtttaaagaaaaaatc
M  T  Q  S  P  I  F  L  T  P  V  F  K  E  K  I

50                    70                    90
tggggcggaaccgctttacgagatagatttggatacagtattccttca
W  G  G  T  A  L  R  D  R  F  G  Y  S  I  P  S

            110                   130
gaatcaacgggggaatgctgggccatttccgctcatccaaaaggaccg
E  S  T  G  E  C  W  A  I  S  A  H  P  K  G  P

   150                   170                   190
agcactgttgcaaatggcccgtataaaggaaagacattgatcgagctt
S  T  V  A  N  G  P  Y  K  G  K  T  L  I  E  L

                  210                   230
tgggaagagcaccgtgaagtattcggcggcgtagaggggatcggttt
W  E  E  H  R  E  V  F  G  G  V  E  G  D  R  F

          250                   270                  2
ccgcttctgacaaagctgctggatgtgaaggaagatacgtcaattaaa
P  L  L  T  K  L  L  D  V  K  E  D  T  S  I  K

90                    310                   330
gttcaccctgatgattactatgccggagaaaacgaagagggagaactc
V  H  P  D  D  Y  Y  A  G  E  N  E  E  G  E  L

            350                   370
ggcaagacggaatgctggtacattatcgactgtaaggaaaacgcagaa
G  K  T  E  C  W  Y  I  I  D  C  K  E  N  A  E

   390                   410                   430
atcatttacgggcatacggcccgctcaaaaaccgaacttgtcacaatg
I  I  Y  G  H  T  A  R  S  K  T  E  L  V  T  M

                  450                   470
atcaacagcggtgactgggagggcctgctgcgaagaatcaaaattaaa
I  N  S  G  D  W  E  G  L  L  R  R  I  K  I  K

          490                   510                  5
ccgggtgatttctattatgtgccgagcggaacgctgcacgcattgtgc
P  G  D  F  Y  Y  V  P  S  G  T  L  H  A  L  C

30                    550                   570
aaggggcccttgttttagagactcagcaaaattcagatgccacatac
K  G  A  L  V  L  E  T  Q  Q  N  S  D  A  T  Y
```

FIG._6A

```
          590                       610
cgggtgtacgattatgaccgtcttgatagcaacggaagtccgagagag
R  V  Y  D  Y  D  R  L  D  S  N  G  S  P  R  E

   630                    650                    670
cttcattttgccaaagcggtcaatgccgccacggttccccatgtggac
L  H  F  A  K  A  V  N  A  A  T  V  P  H  V  D

                690                       710
gggtatatagatgaatcgacagaatcaagaaaaggaataaccattaaa
G  Y  I  D  E  S  T  E  S  R  K  G  I  T  I  K

        730                       750                  7
acatttgtccaaggggaatatttttcggtttataaatgggacatcaat
T  F  V  Q  G  E  Y  F  S  V  Y  K  W  D  I  N

70                    790                       810
ggcgaagctgaaatggctcaggatgaatcctttctgatttgcagcgtg
G  E  A  E  M  A  Q  D  E  S  F  L  I  C  S  V

          830                       850
atagaaggaagcggtttgctcaagtatgaggacaaaacatgtccgctc
I  E  G  S  G  L  L  K  Y  E  D  K  T  C  P  L

   870                    890                    910
aaaaaaggtgatcactttattttgccggctcaaatgcccgattttacg
K  K  G  D  H  F  I  L  P  A  Q  M  P  D  F  T

                930
ataaaaggaacttgtacccttatcgtgtctcatatt
I  K  G  T  C  T  L  I  V  S  H  I
```

FIG._6B